

Amendments to the Specification:

Please replace the paragraph at page 83, line 31 with the following:

Protein identification has been carried out using "PeptIdent" (<http://www.expasy.ch/sprot/peptident.html> provided by the ExPASy Proteomics Server, the Swiss Institute of Bioinformatics). It is a tool that allows the identification of proteins using pI, relative molecular mass and peptide mass fingerprinting data. Experimentally measured, user-specified peptide masses were compared with the theoretical peptides calculated for all proteins in the SWISS-PORT/TREMBL database.

Please replace the paragraph at page 84, line 6 with the following:

When protein identification was not successful with the peptide mass fingerprinting procedure, the supernatant of digested spots was desalted in "ZipTip" C18 pipette tips (Millipore) and eluted with 50% acetonitrile and 0.1% TFA. Peptides were applied by nanoflow (in-house nanospray) sample introduction to a tandem mass spectrometer that consists of two quadrupoles and an orthogonal time of flight tube (Q-TOF) from MicroMass (UK). Fragment ion spectra were interpreted with the MOWSE database search (<http://www.segnet.dl.ac.uk/mowse.thml>).

Please replace the paragraph at page 84, line 19 with the following:

SWISS-2-DPAGE is an annotated 2-D-PAGE database in which all the data are easily retrieved by computer programs and stored in a format similar to that of the SWISS-PORT Protein Sequence Database, one of the most updated and annotated protein sequence databases presently available. The SWISS-2-DPAGE database assembles data on proteins identified on various 2-D-PAGE maps. Each SWISS-2-DPAGE entry contains data on one protein, including mapping procedures, physiological and pathological data and bibliographical references, as well as several 2-D-PAGE images showing the protein location. Cross-references are provided to SWISS-PORT and, through the latter, to other databases (EMBL, Genbank, PROSITE, OMIM, etc). The database has been set up on the ExPASy World Wide Web server (<http://www.expasy.ch/>). Worldwide, scientists using similar 2-D-PAGE protocols (immobilized pH gradient as first dimensional separation) are now able to compare their images with SWISS-2-DPAGE maps.